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            GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      August 6, 2003, 13:01:34 ; Search time 2 seconds
                                        (without alignments)
                                        2.904 Million cell updates/sec

Title:       us-10-036-041-1
Perfect score: 1712
Sequence:    1 ggcatctgcccgaggagacc.........ttgttaaggataaaaaaa 1712

Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 0.5

Searched:    1 seqs, 1696 residues

Total number of hits satisfying chosen parameters:      2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Database :   us-09-552-225a-1:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                        SUMMARIES

                %
Result    Query
No.   Score  Match  Length DB  ID                  Description
----- -----  -----  ------ --  -----------------   -----------
  1   1696    99.1    1696   1  us-09-552-225a-1

                        ALIGNMENTS

RESULT 1
us-09-552-225a-1

Query Match        99.1%;   Score 1696;   DB 1;   Length 1696;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1696;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     9 CCCGAGGAGACCAGCTCCTGGAGCTCTGCGTCTTCAGGGAGACTGCTGGAGGCTCTGAGGCTCTGT   68
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CCCGAGGAGACCACGCTCCTGGAGCTCTGCGTCTTCAGGGAGACTCTGAGGCTCTGT   60

Qy    69 TGGAGAATCATGCTTTGGAGGCAGCTCAGCTGCATCTGCGCCAACTGCCTGGCTTTGTTTTCCTCC  128
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGGAGAATCATGCTTTGGAGGCAGCTCAGCTGCATCTGCGCCAACTGCCTGGCTTTGTTTTCCTCC  120

Qy   129 CTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAG  188
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAG  180

Qy   189 ACTGCAGTAAGTGTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC  248
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ACTGCAGTAAGTGTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC  240

Qy   249 CACCGGGCGCCCCTGGCAATTCCAGGAAACCATGGCAACAATGGCAACAATGGCAGCCACTG  308
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CACCGGGCGCCCCTGGCAATTCCAGGAAACCATGGCAACAATGGCAACAATGGCAGCCACTG  300
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Qy   309 GTCATGAAGGAGCCAAAGGTGAGAAGGGTGACCTGGGCCTGGGGGGAGC  368
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTCATGAAGGAGCCAAAGGTGAGAAGGGTGACCTGGGCCTGGGGGGAGC  360

Qy   369 GGGGGCAGCATGGCCCCAAAGGAGAGGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGA  428
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GGGGGCAGCATGGCCCCAAAGGAGAGGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGA  420

Qy   429 TTGCAATTCATGGCTTCTCTGCCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCA  488
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TTGCAATTCATGGCTTCTCTGCCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCA  480

Qy   489 GCAGTGTTGAGACCAACATTGGAAACTTCTTGATGTCATGACTGGTAGATTGGGGCCC  548
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCAGTGTTGAGACCAACATTGGAAACTTCTTGATGTCATGACTGGTAGATTGGGGCCC  540

Qy   549 CAGTATCAGGTGTATTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAG  608
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CAGTATCAGGTGTGTATTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAG  600

Qy   609 TGTATGTGTACCTTATGCACATGGCAACACAGTCTTCAGCATGTCAGCTATGAAATGA  668
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGTATGTGTACCTTATGCACATGGCAACACAGTCTTCAGCATGTCAGCTATGAAATGA  660

Qy   669 AGGGCAAATCAGATACATCCAGCAATGCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGG  728
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGGCAAATCAGATACATCCAGCAATGCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGG  720

Qy   729 TTTGGCTGCGAATGGCCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTG  788
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TTTGGCTGCGAATGGCCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTG  780

Qy   789 CAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGA  848
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGA  840

Qy   849 AGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACA  908
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACA  900

Qy   909 TTGCTGTATTCAAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAAT  968
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTGCTGTATTCAAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAAT  960

Qy   969 GTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAATAGTCTTCTCAGATGACCTTG  1028
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAATAGTCTTCTCAGATGACCTTG  1020

Qy  1029 ACTAATATACTCAGCATCTTTATCACTCTTTCCTTGCACCTAAAAGATAATTCTCCTCT  1088
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ACTAATATACTCAGCATCTTTATCACTCTTTCCTTGCACCTAAAAGATAATTCTCCTCT  1080

Qy  1089 GACGCAGGTTGGAAATATTTTTTCATCACAGAAGTCATTTGCAAAGAATTTGACTAC  1148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GACGCAGGTTGGAAATATTTTTTCATCACAGAAGTCATTTGCAAAGAATTTGACTAC  1140

Qy  1149 TCTGCTTTTAATTAATACCCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCATTATTCTT  1208
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TCTGCTTTTAATTAATACCCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCATTATTCTT  1200

Qy  1209 TATAACATTTGAGAGAATCGGATGTAGTGATGTGATATGGAGACAGGGCCA  1268
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TATAACATTTGAGAGAATCGGATGTAGTGATGTGATATGGAGACAGGGCCA  1260

Qy  1269 CTAGCTGCCTTATTAGCTAATTTAGTGCCCTCGTGTTAGCCTTGCAGCTTTC  1328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 CTAGCTGCCTTATTAGCTAATTTAGTGCCCTCGTGTTAGCCTTGCAGCTTTC  1320

Qy  1329 CTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCA  1388
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCA  1380

Qy  1389 ATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGCTGGTTGTAATGTGTTGTATGTTCCC  1448
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Db    1381 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1440
           ATAGATTTTAGCTATAAAGTGCTTGACCAGTAAGTGGTTGTAATTTTGTATGTTCCC

Qy    1449 CCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATG 1508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATG 1500

Qy    1509 TCATAAATATCTCATAGAGAGTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAG 1568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TCATAAATATCTCATAGAGAGTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAG 1560

Qy    1569 AGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAGATTTTGAC 1628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 AGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAGATTTTGAC 1620

Qy    1629 CTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACAC 1688
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 CTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACAC 1680

Qy    1689 ACCTTTGTTAAAGATA 1704
           ||||||||||||||||
Db    1681 ACCTTTGTTAAAGATA 1696
```

Search completed: August 6, 2003, 13:01:36
Job time : 2 secs

Search completed: August 6, 2003, 13:03:18
Job time : 0.001 secs

OM protein - protein search, using sw model

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Run on: August 6, 2003, 13:03:18 ; Search time 0.001 Seconds
                                           (without alignments)
                                           60.516 Million cell updates/sec

Title: us-10-036-041-2
Perfect score: 1367
Sequence: 1 MLWRQLIYWQLLALFFLPFC..........LHGDHQRFSTFAGFLLFETK 246

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 246 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Database :   us-09-552-225a-2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                                  %
Result   Query
No.   Score   Match Length DB ID   Description
------ -----   ----- ------ -- -------------------------- -----------
  1   1367   100.0   246   1 us-09-552-225a-2

                             ALIGNMENTS

RESULT 1
us-09-552-225a-2

Query Match   100.0%;   Score 1367;   DB 1; Length 246;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 246;   Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG 60

Qy   61 PPGIPGNHGNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PPGIPGNHGNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120

Qy   121 MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV 180

Qy   181 YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF 240

Qy   241 LLFETK 246
         ||||||
Db   241 LLFETK 246